

AMENDMENT TO THE CLAIMS

Claims 1-10 (Cancelled)

11. (Currently Amended) An isolated cDNA molecule of Claim 8 that consists of the nucleic acid sequence set forth in SEQ ID NO:1.

12. (Cancelled)

13. (Withdrawn) An isolated genomic DNA molecule that: (a) encodes a CAN-1 polypeptide; (b) is less than 38 kilobases long; and (c) hybridizes to the complement of the nucleic acid molecule of SEQ ID NO:1 under conditions of 2 X SSC at 55°C for 30 minutes.

14. (Withdrawn) An isolated genomic DNA molecule of Claim 13 that hybridizes to the complement of the nucleic acid molecule of SEQ ID NO:1 under conditions of 1 X SSC at 55°C for 30 minutes.

15. (Withdrawn) An isolated genomic DNA molecule of Claim 13 that hybridizes to the complement of the nucleic acid molecule of SEQ ID NO:1 under conditions of 0.2 X SSC at 55°C for 30 minutes.

16. (Cancelled)

17. (Withdrawn) An isolated genomic DNA molecule that:

(a) encodes a CAN-1 polypeptide;

(b) comprises a nucleic acid sequence that is at least 70% identical to the CAN-1 genomic DNA sequence set forth in SEQ ID NO:4; and

(c) comprises at least one of the single nucleotide polymorphisms set forth in Table 1 herein.

18. (Withdrawn) An isolated genomic DNA molecule that:

(a) encodes a CAN-1 polypeptide;

(b) comprises a nucleic acid molecule that hybridizes to the complement of the CAN-1 genomic DNA sequence set forth in SEQ ID NO:4 under conditions of 2 X SSC at 55°C for 30 minutes; and

(c) comprises the nucleic acid sequence TTACAG at positions 7 through 12 of the nucleic acid molecule that hybridizes to the complement of the CAN-1 genomic DNA sequence set forth in SEQ ID NO:4 under conditions of 2 X SSC at 55°C for 30 minutes.

19. (Cancelled)

20. (Withdrawn) An isolated nucleic acid molecule that encodes an STG protein and that hybridizes under conditions of 2 X SSC at 55°C for 30 minutes to the complement of the cDNA molecule set forth in SEQ ID NO:5, provided that the isolated nucleic acid molecule is not a genomic DNA molecule greater than 43 kilobases long.

21. (Withdrawn) An isolated cDNA molecule of Claim 20.

22. (Withdrawn) An isolated genomic DNA molecule of Claim 20.

23. (Withdrawn) An isolated cDNA molecule that:

(a) encodes an STG polypeptide that is the same length as the STG polypeptide consisting of the amino acid sequence of SEQ ID NO:6, wherein the encoded STG polypeptide is at least 70% identical to the STG polypeptide consisting of the amino acid sequence set forth in SEQ ID NO:6; and

(b) includes a single nucleotide polymorphism selected from the group consisting of: the first nucleic acid residue of the forty eighth codon is A; the second nucleic acid residue of the eighty first codon is C; the first nucleic acid residue of the eighty third codon is C; the third nucleic acid residue of the one hundred and sixty fourth codon is T; the first nucleic acid residue of the one hundred and sixty fifth codon is A; and the third nucleic acid residue of the three hundredth codon is C.

24. (Withdrawn) An isolated genomic DNA molecule that:

(a) encodes an STG polypeptide;

(b) comprises a nucleic acid sequence that is at least 70% identical to the STG genomic DNA sequence set forth in SEQ ID NO:7; and

(c) comprises at least one of the single nucleotide polymorphisms set forth in Table 2 herein.

25. (Withdrawn) An isolated oligonucleotide, between 10 base pairs and 100 base pairs in length, that hybridizes at 10°C below its melting temperature to the STG cDNA of SEQ ID NO:5, or to the STG genomic clone of SEQ ID NO:7, or to the complement of the STG cDNA of SEQ ID NO:5, or to the complement of the STG genomic clone of SEQ ID NO:7.

26. (Currently Amended) *An isolated* A vector comprising a nucleic acid molecule of Claim 11, Claim 8, Claim 13 or Claim 20.

- 3
27. (Original) ~~A~~ host cell comprising a vector of Claim 26.
28. (Withdrawn) An isolated CAN-1 polypeptide that is at least 70% identical to the CAN-1 polypeptide of SEQ ID NO:2, or is at least 70% identical to the CAN-1 polypeptide of SEQ ID NO:3.
29. (Withdrawn) An isolated CAN-1 polypeptide of Claim 28 that is at least 70% identical to the CAN-1 polypeptide of SEQ ID NO:2.
30. (Withdrawn) An isolated CAN-1 polypeptide of Claim 28 that is at least 70% identical to the CAN-1 polypeptide of SEQ ID NO:3.
31. (Withdrawn) An isolated SEEK-1 polypeptide that is at least 70% identical to the SEEK-1 polypeptide of SEQ ID NO:9.
32. (Withdrawn) An isolated STG polypeptide that is at least 70% identical to the STG polypeptide of SEQ ID NO:6.
33. (Withdrawn) An isolated antibody that binds specifically to a polypeptide consisting of an amino acid sequence that is at least 70% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:6, and SEQ ID NO:9.
34. (Withdrawn) An isolated antibody of Claim 33 that binds specifically to a polypeptide that is at least 70% identical to the polypeptide having the amino acid sequence set forth in SEQ ID NO:2.
35. (Withdrawn) An isolated antibody of Claim 34, wherein said antibody is a monoclonal antibody.
36. (Withdrawn) An isolated antibody of Claim 34, wherein said antibody is a polyclonal antibody.
37. (Withdrawn) An isolated antibody of Claim 34, wherein said antibody is a CDR-grafted antibody.
38. (Withdrawn) An isolated antibody of Claim 33 that binds specifically to a polypeptide that is at least 70% identical to the polypeptide having the amino acid sequence set forth in SEQ ID NO:3.
39. (Withdrawn) An isolated antibody of Claim 38, wherein said antibody is a monoclonal antibody.

40. (Withdrawn) An isolated antibody of Claim 38, wherein said antibody is a polyclonal antibody.
41. (Withdrawn) An isolated antibody of Claim 38, wherein said antibody is a CDR-grafted antibody.
42. (Withdrawn) An isolated antibody of Claim 33 that binds specifically to a polypeptide that is at least 70% identical to the polypeptide having the amino acid sequence set forth in SEQ ID NO:6.
43. (Withdrawn) An isolated antibody of Claim 42, wherein said antibody is a monoclonal antibody.
44. (Withdrawn) An isolated antibody of Claim 42, wherein said antibody is a polyclonal antibody.
45. (Withdrawn) An isolated antibody of Claim 42, wherein said antibody is a CDR-grafted antibody.
46. (Withdrawn) An isolated antibody of Claim 33 that binds specifically to a polypeptide that is at least 70% identical to the polypeptide having the amino acid sequence set forth in SEQ ID NO:9.
47. (Withdrawn) An isolated antibody of Claim 46, wherein said antibody is a monoclonal antibody.
48. (Withdrawn) An isolated antibody of Claim 46, wherein said antibody is a polyclonal antibody.
49. (Withdrawn) An isolated antibody of Claim 46, wherein said antibody is a CDR-grafted antibody.
50. (Withdrawn) A method of diagnosing or predicting the susceptibility to psoriasis in an individual, said method comprising the steps of:
- (a) obtaining a sample from an individual;
 - (b) determining an expression level of at least one polypeptide chosen from the group consisting of CAN-1, STG, and SEEK-1 in said sample; and
 - (c) diagnosing or predicting the susceptibility of said individual to psoriasis based on the presence or amount of expression of said polypeptide.
51. (Withdrawn) A method for ameliorating the symptoms and/or progression of psoriasis, the method comprising the step of administering to an

individual suffering from psoriasis an inhibitory amount of a selective inhibitor of a polypeptide chosen from the group consisting of CAN-1, STG and SEEK-1, wherein the inhibitory amount of the selective inhibitor causes a reduction in the amount and/or activity of the polypeptide.

~~4~~ ~~52.~~ (Currently Amended) A method of making an isolated CAN-1, STG or ~~SEEK-1~~ polypeptide comprising:

- (a) culturing a host cell comprising a vector comprising a nucleic acid molecule of SEQ ID NO:1 encoding a CAN-1, ~~STG or SEEK-1~~ polypeptide under conditions that enable expression of said CAN-1, ~~STG or SEEK-1~~ polypeptide; and
- (b) recovering said expressed polypeptide.

53. (Withdrawn) A method for identifying a binding partner to a CAN-1, STG or SEEK-1 polypeptide comprising:

- (a) contacting a CAN-1, STG or SEEK-1 polypeptide with a binding partner; and
- (b) determining whether the binding partner affects an activity of the polypeptide.

54. (Withdrawn) A method of inhibiting movement of cells into the epidermis comprising contacting a CAN-1 binding partner to a CAN-1 polypeptide such that the binding partner inhibits movement of cells into the epidermis by reducing a chemotactic property of the CAN-1 polypeptide.

55. (Withdrawn) The method of Claim 54 wherein said cells are selected from a group consisting of T-cells, endothelial cells, lymphocytes, monocytes and neutrophils.

56. (Withdrawn) A method of inhibiting hyperproliferation of keratinocytes comprising contacting a CAN-1 binding partner to a CAN-1 polypeptide such that the binding partner inhibits the hyperproliferation of keratinocytes by reducing a hyperproliferation property of the CAN-1 polypeptide.

57. (Withdrawn) A method of inhibiting abnormal differentiation of keratinocytes comprising contacting a CAN-1 binding partner to a CAN-1 polypeptide such that the binding partner inhibits abnormal differentiation of keratinocytes by reducing an amount of unbound CAN-1.

80% of the nucleic acid residues in the 100 base pair candidate portion align with the identical nucleic acid residues in the 100 base pair subject nucleic acid sequence, then the 100 base pair candidate portion of the larger DNA molecule is 80% identical to the subject nucleic acid sequence.

- 5 Nucleic acid sequence identity can be determined in the following manner. The subject nucleic acid sequence is used to search a nucleic acid sequence database, such as the GenBank database (accessible at web site ^{World Wide Web} <http://www.ncbi.nlm.nih.gov/blast/>), using the program BLASTM version 2.1 (based on Altschul et al., Nucleic Acids Research 25:3389-3402 (1997)). The program is used in the ungapped mode. Default filtering is used to remove sequence homologies due to regions of low complexity. The default parameters of BLASTM are utilized.

my 7-2-05
see
Examiner's
Amendment

- 10 Amino acid sequence identity can be determined in the following manner. The subject polypeptide sequence is used to search a polypeptide sequence database, such as the GenBank database (accessible at web site ^{World Wide Web} <http://www.ncbi.nlm.nih.gov/blast/>), using the BLASTP program. The program is used in the ungapped mode. Default filtering is used to remove sequence homologies due to regions of low complexity. The default parameters of BLASTP are utilized. Filtering for sequences of low complexity utilize the SEG program.

my 7-2-05
see
Examiner's
Amendment

- 20 The term "hybridize under stringent conditions", and grammatical equivalents thereof, refers to the ability of a nucleic acid molecule to hybridize to a target nucleic acid molecule (such as a target nucleic acid molecule immobilized on a DNA or RNA blot, such as a Southern blot or Northern blot) under defined conditions of temperature and salt concentration. With respect to nucleic acid molecules greater than about 100 bases in length, typical stringent hybridization conditions are no more than 25°C to 30°C (for example, 10°C) below the melting temperature (T_m) of the native duplex (*see generally*, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed. Cold Spring Harbor Press, 1987; Ausubel et al., *Current Protocols in Molecular Biology*, Greene Publishing, 1987). T_m for nucleic acid molecules greater than about 100 bases can be calculated by the formula $T_m = 81.5 + 0.41\% (G + C - \log (Na^+))$.

- 30 With respect to nucleic acid molecules having a length less than 100 bases, exemplary stringent hybridization conditions are 5° to 10°C below T_m .